

NiceProt View of Swiss-Prot: P08253NiceProt View of Swiss-Prot: P08253

General information about the entry



Entry nameMM02_HUMAN
Primary accession numberP08253
Secondary accession numbersNone
Entered in Swiss-Prot inRelease 08, August 1988
Sequence was last modified inRelease 17, February 1991
Annotations were last modified in Release 42, September 2003
Name and origin of the protein

Protein name72 kDa type IV collagenase [Precursor]
SynonymsSEC 3.4.24.24
72 kDa gelatinase
Matrix metalloproteinase-2
MMP-2
Gelatinase A
TBE-1
Gene nameMMP2 or CLG4A

FromHomo sapiens (Human) [TaxID: 9606]

TaxonomyEukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
Homo.

References

- [1]
SEQUENCE OF 19-660 FROM NUCLEIC ACID, AND PARTIAL SEQUENCE.
MEDLINE=88198218; PubMed=2834383;
Collier I.E., Wilhelm S.M., Eisen A.Z., Marmer B.L., Grant G.A.,
Seltzer J.L., Kronberger A., He C., Bauer E.A., Goldberg G.I.;
"H-ras oncogene-transformed human bronchial epithelial cells (TBE-1)
secrete a single metalloprotease capable of degrading basement
membrane collagen.";
J. Biol. Chem. 263:6579-6587(1988).
- [2]
SEQUENCE FROM NUCLEIC ACID.
MEDLINE=91236162; PubMed=1851724;
Collier I.E., Bruns G.A.P., Goldberg G.I., Gerhard D.S.;
"On the structure and chromosome location of the 72- and 92-kDa
human type IV collagenase genes.";
Genomics 9:429-434(1991).
- [3]
SEQUENCE FROM NUCLEIC ACID.
MEDLINE=90293047; PubMed=2162831;
Huhtala P., Chow L.T., Tryggvason K.;
"Structure of the human type IV collagenase gene.";
J. Biol. Chem. 265:11077-11082(1990).
- [4]
SEQUENCE FROM NUCLEIC ACID.
TISSUE=Brain;
MEDLINE=22388257; PubMed=12477932;

Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D., Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K., Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F., Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E., Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C., Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J., Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A., Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S., Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E., Jones S.J., Marra M.A.;

"Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences.";

Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).

[5]

SEQUENCE OF 1-51 FROM NUCLEIC ACID.

MEDLINE=90228972; PubMed=2158484;

Huhtala P., Eddy R.L., Fan Y.S., Byers M.G., Shows T.B., Tryggvason K.;

"Completion of the primary structure of the human type IV collagenase preproenzyme and assignment of the gene (CLG4) to the q21 region of chromosome 16.";

Genomics 6:554-559(1990).

[6]

X-RAY CRYSTALLOGRAPHY (2.15 ANGSTROMS) OF 443-660.

MEDLINE=96069777; PubMed=7583664;

Libson A.M., Gittis A.G., Collier I.E., Marmer B.L., Goldberg G.I., Lattman E.E.;

"Crystal structure of the haemopexin-like C-terminal domain of gelatinase A.";

Nat. Struct. Biol. 2:938-942(1995).

[7]

X-RAY CRYSTALLOGRAPHY (2.6 ANGSTROMS) OF 458-660.

MEDLINE=96140723; PubMed=8549817;

Gohlke U., Gomis-Ruth F.X., Crabbe T., Murphy G., Docherty A.J., Bode W.;

"The C-terminal (haemopexin-like) domain structure of human gelatinase A (MMP2): structural implications for its function.";

FEBS Lett. 378:126-130(1996).

Comments

CATALYTIC ACTIVITY: Cleavage of gelatin type I and collagen types IV, V, VII, X. Cleaves the collagen-like sequence

Pro-Gln-Gly-|-Ile-Ala-Gly-Gln.

COFACTOR: REQUIRES CALCIUM AND ZINC FOR ACTIVITY.

SUBUNIT: LIGAND FOR INTEGRIN ALPHA-V/BETA-3.

TISSUE SPECIFICITY: PRODUCED BY NORMAL SKIN FIBROBLASTS.
PTM: The propeptide is processed by MMP14 (MT-MMP1) and MMP16 (MT-MMP3).

SIMILARITY: BELONGS TO PEPTIDASE FAMILY M10A.
SIMILARITY: Contains 1 hemopexin-like domain.
SIMILARITY: Contains 3 fibronectin type II domains.

Copyright

This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <http://www.isb-sib.ch/announce/> or send an email to license@isb-sib.ch)

Cross-references

EMBLJ03210; AAA35701.1; -.
M33789; AAA52027.1; -.
M55593; AAA52028.1; -.
M58552; AAA52028.1; JOINED.
M55582; AAA52028.1; JOINED.
M55583; AAA52028.1; JOINED.
M55584; AAA52028.1; JOINED.
M55585; AAA52028.1; JOINED.
M55586; AAA52028.1; JOINED.
M55587; AAA52028.1; JOINED.
M55588; AAA52028.1; JOINED.
M55589; AAA52028.1; JOINED.
M55590; AAA52028.1; JOINED.
M55591; AAA52028.1; JOINED.
M55592; AAA52028.1; JOINED.
BC002576; AAH02576.1; -.

PIRA28153; A28153.

PDB1RTG; 10-JUN-96.

1GEN; 17-AUG-96.

Detailed list of linked structures.

MEROPSM10.003; -.

GenewHGNC:7166; MMP2.

CleanExHGNC:7166; MMP2.

MIM120360 .

GeneCardsMMP2.

GeneLynxMMP2; Homo sapiens.

GOGO:0005615; Cellular component: immunoglobulin complex,
circulating (traceable author statement).

GO:0004228; Molecular function: gelatinase A activity
(traceable author statement).

GO:0008270; Molecular function: zinc ion binding activity
(traceable author statement).

InterProIPR000562; FN_Type_II.

IPR000585; Hemopexin.

IPR001818; Matrixin.

IPR006026; NZn_MTpeptdse.

IPR006025; Zn_MTpeptdse.

PfamPF00040; fn2; 3.
 PF00045; hemopexin; 4.
 PF00413; Peptidase_M10; 1.
 PF03933; Peptidase_M10_N; 1.
 PRINTSPR00013; FNTYPEII.
 PR00138; MATRIXIN.
 ProDomPD000995; FN_Type_II; 3.
 [Domain structure / List of seq. sharing at least 1 domain].
 SMARTSM00059; FN2; 3.
 SM00120; HX; 4.
 SM00235; ZnMc; 1.
 PROSITEPS00023; FIBRONECTIN_2; 3.
 PS00024; HEMOPEXIN; 1.
 PS00142; ZINC_PROTEASE; 1.
 PS00546; CYSTEINE_SWITCH; 1.
 Implicit links toSOURCE; Ensembl; BLOCKS; ProtoNet; ProtoMap;
 PRESAGE; DIP; ModBase; SWISS-2DPAGE.

Keywords

Hydrolase; Metalloprotease; Glycoprotein; Zinc; Zymogen; Calcium;
 Collagen degradation; Extracellular matrix; Repeat; Signal;
 3D-structure.

Features

KeyFrom	To	Length	Description
SIGNAL	1	29 29	POTENTIAL.
PROPEP	30	109 80	ACTIVATION PEPTIDE.
CHAIN	110	660 551	72 kDa TYPE IV COLLAGENASE.
DOMAIN	110	221 112	COLLAGENASE-LIKE 1.
DOMAIN	222	396 175	COLLAGEN-BINDING.
DOMAIN	397	465 69	COLLAGENASE-LIKE 2.
DOMAIN	226	283 58	FIBRONECTIN TYPE-II 1.
DOMAIN	284	341 58	FIBRONECTIN TYPE-II 2.
DOMAIN	342	399 58	FIBRONECTIN TYPE-II 3.
DOMAIN	466	660 195	HEMOPEXIN-LIKE.
SITE	102	102 1	CYSTEINE SWITCH (POTENTIAL).
METAL	403	403	ZINC (CATALYTIC) (BY SIMILARITY).
ACT_SITE	404	404	BY SIMILARITY.
METAL	407	407	ZINC (CATALYTIC) (BY SIMILARITY).
METAL	413	413	ZINC (CATALYTIC) (BY SIMILARITY).
CARBOHYD	573	573	N-LINKED (GLCNAC...) (POTENTIAL).
CARBOHYD	642	642	N-LINKED (GLCNAC...) (POTENTIAL).
DISULFID	469	660	
TURN	468	470 3	
STRAND	477	481 5	
TURN	482	483 2	
STRAND	484	489 6	
TURN	490	491 2	
STRAND	492	496 5	
TURN	499	500 2	
STRAND	504	508 5	
HELIX	509	511 3	
TURN	512	512 1	
TURN	514	515 2	

```

STRAND  522    526    5
TURN    527    530    4
STRAND  531    536    6
TURN    537    538    2
STRAND  539    544    6
TURN    545    546    2
STRAND  547    548    2
TURN    550    551    2
STRAND  554    555    2
HELIX   556    559    4
TURN    560    560    1
TURN    563    564    2
STRAND  570    574    5
TURN    575    578    4
STRAND  579    584    6
TURN    585    586    2
STRAND  587    592    6
TURN    593    596    4
STRAND  597    598    2
STRAND  604    605    2
HELIX   606    609    4
STRAND  619    622    4
TURN    624    626    3
STRAND  628    633    6
TURN    634    635    2
STRAND  636    641    6
TURN    642    643    2
STRAND  644    652    9
HELIX   653    656    4
TURN    657    657    1

```

Sequence information

Length: 660 AA [This is the length of the unprocessed precursor]
 Molecular weight: 73882 Da [This is the MW of the unprocessed precursor]
 CRC64: BC7147DC8B49F289 [This is a checksum on the sequence]

```

      10      20      30      40      50      60
      |      |      |      |      |      |
MEALMARGAL TGPLRALCLL GCLLSHAAAA PSPIIKFPGD VAPKTDKELA VQYLNTFYGC

      70      80      90     100     110     120
      |      |      |      |      |      |
PKESCNLFVL KDTLKKMQKF FGLPQTGDLD QNTIETMRKP RCGNPDVANY NFFPRKPKWD

     130     140     150     160     170     180
      |      |      |      |      |      |
KNQITYRIIG YTPDLDPETV DDAFARAFQV WSDVTPLRFS RIHDGEADIM INFGRWEHGD

     190     200     210     220     230     240
      |      |      |      |      |      |
GYPFDGKDGL LAHAFAPGTG VGGDSHFDDD ELWTLGEGQV VRVKYGNADG EYCKFPFLFN

     250     260     270     280     290     300
      |      |      |      |      |      |

```

GKEYNSCTDT GRSDGFLWCS TTYNFEKDGK YGFCPHEALF TMGGNAEGQP CKFPFRFQGT

310	320	330	340	350	360
SYDSCTTEGR	TDGYRWCGTT	EDYDRDKKYG	FCPETAMSTV	GGNSEGAPCV	FPFTFLGNKY

370	380	390	400	410	420
ESCTSAGRSD	GKMWCATTAN	YDDDRKWGFC	PDQGYSFLV	AAHEFGHAMG	LEHSQDPGAL

430	440	450	460	470	480
MAPIYTYTKN	FRLSQDDIKG	IQELYGASPD	IDLGTGPTPT	LGPVTPEICK	QDIVFDGIAQ

490	500	510	520	530	540
IRGEIFFFKD	RFIWRTVTPR	DKPMGPLLVA	TFWPELPEKI	DAVYEAPQEE	KAVFFAGNEY

550	560	570	580	590	600
WIYSASTLER	GYPKPLTSLG	LPPDVQRVDA	AFNWSKNKKT	YIFAGDKFWR	YNEVKKKMDP

610	620	630	640	650	660
GFPKLIADAW	NAIPDNLDAV	VDLQGGGHSY	FFKGAYYLLK	ENQSLKSVKF	GSIKSDWLGC

NiceProt View of Swiss-Prot: P14780NiceProt View of Swiss-Prot: P14780
General information about the entry



Entry nameMM09_HUMAN
Primary accession numberP14780
Secondary accession numberQ9H4Z1
Entered in Swiss-Prot inRelease 14, April 1990
Sequence was last modified inRelease 14, April 1990
Annotations were last modified in Release 42, September 2003
Name and origin of the protein

Protein name92 kDa type IV collagenase [Precursor]
SynonymsSEC 3.4.24.35
92 kDa gelatinase
Matrix metalloproteinase-9
MMP-9
Gelatinase B
GELB
Gene nameMMP9 or CLG4B

FromHomo sapiens (Human) [TaxID: 9606]

TaxonomyEukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
Homo.

References

- [1]
SEQUENCE FROM NUCLEIC ACID, AND SEQUENCE OF 20-37.
MEDLINE=90008879; PubMed=2551898;
Wilhelm S.M., Collier I.E., Marmer B.L., Eisen A.Z., Grant G.A.,
Goldberg G.I.;
"SV40-transformed human lung fibroblasts secrete a 92-kDa type IV
collagenase which is identical to that secreted by normal human
macrophages.";
J. Biol. Chem. 264:17213-17221(1989).
- [2]
SEQUENCE FROM NUCLEIC ACID.
MEDLINE=91358433; PubMed=1653238;
Huhtala P., Tuuttila A., Chow L.T., Lohi J., Keski-Oja J.,
Tryggvason K.;
"Complete structure of the human gene for 92-kDa type IV
collagenase. Divergent regulation of expression for the 92- and
72-kilodalton enzyme genes in HT-1080 cells.";
J. Biol. Chem. 266:16485-16490(1991).
- [3]
SEQUENCE FROM NUCLEIC ACID.
MEDLINE=21638749; PubMed=11780052;
Deloukas P., Matthews L.H., Ashurst J., Burton J., Gilbert J.G.R.,
Jones M., Stavrides G., Almeida J.P., Babbage A.K., Bagguley C.L.,
Bailey J., Barlow K.F., Bates K.N., Beard L.M., Beare D.M., Beasley
O.P., Bird C.P., Blakey S.E., Bridgeman A.M., Brown A.J., Buck D.,
Burrill W.D., Butler A.P., Carder C., Carter N.P., Chapman J.C.,
Clamp M., Clark G., Clark L.N., Clark S.Y., Clee C.M., Clegg S.,

Cobley V.E., Collier R.E., Connor R.E., Corby N.R., Coulson A., Coville G.J., Deadman R., Dhami P.D., Dunn M., Ellington A.G., Frankland J.A., Fraser A., French L., Garner P., Grafham D.V., Griffiths C., Griffiths M.N.D., Gwilliam R., Hall R.E., Hammond S., Harley J.L., Heath P.D., Ho S., Holden J.L., Howden P.J., Huckle E., Hunt A.R., Hunt S.E., Jekosch K., Johnson C.M., Johnson D., Kay M.P., Kimberley A.M., King A., Knights A., Laird G.K., Lawlor S., Lehvaeslaiho M.H., Liversha M.A., Lloyd C., Lloyd D.M., Lovell J.D., Marsh V.L., Martin S.L., McConnachie L.J., McLay K., McMurray A.A., Milne S.A., Mistry D., Moore M.J.F., Mullikin J.C., Nickerson T., Oliver K., Parker A., Patel R., Pearce T.A.V., Peck A.I., Phillimore B.J.C.T., Prathalingam S.R., Plumb R.W., Ramsay H., Rice C.M., Ross M.T., Scott C.E., Sehra H.K., Shownkeen R., Sims S., Skuce C.D., Smith M.L., Soderlund C., Steward C.A., Sulston J.E., Swann R.M., Sycamore N., Taylor R., Tee L., Thomas D.W., Thorpe A., Tracey A., Tromans A.C., Vaudin M., Wall M., Wallis J.M., Whitehead S.L., Whittaker P., Willey D.L., Williams L., Williams S.A., Wilming L., Wray P.W., Hubbard T., Durbin R.M., Bentley D.R., Beck S., Rogers

J.;

"The DNA sequence and comparative analysis of human chromosome 20.";
Nature 414:865-871(2001).

[4]

SEQUENCE FROM NUCLEIC ACID.

TISSUE=B-cell;

MEDLINE=22388257; PubMed=12477932;

Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D., Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K., Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F., Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E., Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C., Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J., Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A., Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S., Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E., Jones S.J., Marra M.A.;

"Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences.";

Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).

[5]

SEQUENCE OF 1-11 FROM NUCLEIC ACID.

MEDLINE=93149601; PubMed=8426746;

Sato H., Seiki M.;

"Regulatory mechanism of 92 kDa type IV collagenase gene expression which is associated with invasiveness of tumor cells.";

Oncogene 8:395-405(1993).

[6]

SEQUENCE OF 20-37.

MEDLINE=91355647; PubMed=1653055;
van Ranst M., Norga K., Masure S., Proost P., Vandekerckhove F.,
Auwerx J., van Damme J., Opdenakker G.;
"The cytokine-protease connection: identification of a 96-kD THP-1
gelatinase and regulation by interleukin-1 and cytokine inducers.";
Cytokine 3:231-239(1991).

[7]

SEQUENCE OF 28-60.
TISSUE=Neutrophils;
MEDLINE=91249834; PubMed=1645657;
Masure S., Proost P., van Damme J., Opdenakker G.;
"Purification and identification of 91-kDa neutrophil gelatinase.
Release by the activating peptide interleukin-8.";
Eur. J. Biochem. 198:391-398(1991).

[8]

CHARACTERIZATION.
Kang K., Lee D.-H.;
"Purification and characterization of human 92-kDa type IV
collagenase (gelatinase B).";
Exp. Mol. Med. 28:161-165(1996).

[9]

3D-STRUCTURE MODELING.
Mallena S.C., Sagajkar R.D.;
"Theoretical model of human type IV collagenase precursor.";
Submitted (APR-2002) to the PDB data bank.

[10]

VARIANTS VAL-20; LYS-82 AND GLN-279.
MEDLINE=20065865; PubMed=10598806;
Zhang B., Henney A., Eriksson P., Hamsten A., Watkins H., Ye S.;
"Genetic variation at the matrix metalloproteinase-9 locus on
chromosome 20q12.2-13.1.";
Hum. Genet. 105:418-423(1999).

Comments

FUNCTION: COULD PLAY A ROLE IN BONE OSTEOCLASTIC RESORPTION.
CATALYTIC ACTIVITY: Cleavage of gelatin types I and V and collagen types
IV and V.
COFACTOR: Binds 2 zinc ions per subunit, calcium (By similarity).
SUBUNIT: EXISTS AS MONOMER, DISULFIDE-LINKED HOMODIMER, AND AS A
HETERODIMER WITH A 25 kDa PROTEIN. MACROPHAGES AND TRANSFORMED CELL
LINES PRODUCE ONLY THE MONOMERIC FORM.
TISSUE SPECIFICITY: PRODUCED BY NORMAL ALVEOLAR MACROPHAGES AND
GRANULOCYTES.
SIMILARITY: THE CENTRAL DOMAIN SHOWS SIMILARITY TO THE TYPE-II MOTIF OF
COLLAGEN-BINDING DOMAIN OF FIBRONECTIN. THIS DOMAIN BINDS GELATIN.
SIMILARITY: BELONGS TO PEPTIDASE FAMILY M10A.
SIMILARITY: Contains 1 hemopexin-like domain.
SIMILARITY: Contains 3 fibronectin type II domains.

Copyright

This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <http://www.isb-sib.ch/announce/> or send an email to license@isb-sib.ch)

Cross-references

EMBLJ05070; AAA51539.1; -.

D10051; BAA20967.1; -.

AL162458; CAC10459.1; -.

BC006093; AAH06093.1; -.

PIRA34458; A34458.

S16097; S16097.

PDB1LKG; 15-MAY-02.

MEROPSM10.004; -.

GlycoSuiteDBP14780; -.

GenewHGNC:7176; MMP9.

CleanExHGNC:7176; MMP9.

MIM120361 .

GeneCardsMMP9.

GeneLynxMMP9; Homo sapiens.

GOGO:0005615; Cellular component: immunoglobulin complex,
circulating (traceable author statement).

GO:0008133; Molecular function: collagenase activity
(traceable author statement).

GO:0008270; Molecular function: zinc ion binding activity
(traceable author statement).

InterProIPR000562; FN_Type_II.

IPR000585; Hemopexin.

IPR001818; Matrixin.

IPR006026; NZn_MTpeptdse.

IPR006970; PT.

IPR006025; Zn_MTpeptdse.

PfamPF00040; fn2; 3.

PF00045; hemopexin; 4.

PF00413; Peptidase_M10; 1.

PF03933; Peptidase_M10_N; 1.

PF04886; PT; 1.

PRINTSPR00013; FNTYPEII.

PR00138; MATRIXIN.

ProDomPD000995; FN_Type_II; 3.

[Domain structure / List of seq. sharing at least 1 domain].

SMARTSM00059; FN2; 3.

SM00120; HX; 4.

SM00235; ZnMc; 1.

PROSITEPS00142; ZINC_PROTEASE; 1.

PS00023; FIBRONECTIN_2; 3.

PS00024; HEMOPEXIN; 1.

PS00546; CYSTEINE_SWITCH; 1.

Implicit links toSOURCE; Ensembl; BLOCKS; ProtoNet; ProtoMap;

PRESAGE; DIP; ModBase; SWISS-2DPAGE.

Keywords

Hydrolase; Metalloprotease; Glycoprotein; Zinc; Zymogen; Calcium;
Collagen degradation; Extracellular matrix; Repeat; Signal;
Polymorphism; 3D-structure.

Features

Key	From	To	Length	Description	FTId
SIGNAL	1	19	19		
PROPEP	20	106	87	ACTIVATION PEPTIDE.	
CHAIN	107	707	601	92 kDa TYPE IV COLLAGENASE.	
DOMAIN	223	280	58	FIBRONECTIN TYPE-II 1.	
DOMAIN	281	339	59	FIBRONECTIN TYPE-II 2.	
DOMAIN	340	397	58	FIBRONECTIN TYPE-II 3.	
DOMAIN	513	707	195	HEMOPEXIN-LIKE.	
SITE	99	99	1	CYSTEINE SWITCH (BY SIMILARITY).	
METAL	401	401		ZINC (CATALYTIC) (BY SIMILARITY).	
ACT_SITE	402	402		BY SIMILARITY.	
METAL	405	405		ZINC (CATALYTIC) (BY SIMILARITY).	
METAL	411	411		ZINC (CATALYTIC) (BY SIMILARITY).	
CARBOHYD	38	38		N-LINKED (GLCNAC...) (POTENTIAL).	
CARBOHYD	120	120		N-LINKED (GLCNAC...) (POTENTIAL).	
CARBOHYD	127	127		N-LINKED (GLCNAC...) (POTENTIAL).	
DISULFID	516	704		BY SIMILARITY.	
VARIANT	20	20		A -> V (IN dbSNP:1805088)	
[NCBI/Ensembl]. VAR_013780					
VARIANT	82	82		E -> K (IN dbSNP:1805089)	
[NCBI/Ensembl]. VAR_013781					
VARIANT	279	279		R -> Q (COMMON POLYMORPHISM;	
dbSNP:17576) [NCBI/Ensembl]. VAR_013782					
VARIANT	668	668		R -> Q (IN dbSNP:17577)	
[NCBI/Ensembl]. VAR_014742					
CONFLICT	574	574		P -> R (IN REF. 3).	

Sequence information

Length: 707 AA [This is the length of the unprocessed precursor]
Molecular weight: 78427 Da [This is the MW of the unprocessed precursor]
CRC64: FB5483E9B9FF2AE8 [This is a checksum on the sequence]

10	20	30	40	50	60
MSLWQPLVLV	LLVLGCCFAA	PRQRQSTLVL	FPGDLRTNLT	DRQLAEEYLY	RYGYTRVAEM
70	80	90	100	110	120
RGESKSLGPA	LLLLQQLSL	PETGELDSAT	LKAMRTPRCG	VPDLGRFQTF	EGDLKWHHHN
130	140	150	160	170	180
ITYWIQNYSE	DLPRAVIDDA	FARAFALWSA	VTPLTFTRVY	SRDADIVIQF	GVAEHGDGYP
190	200	210	220	230	240

FDGKDGLLAH	AFPPGPGIQG	DAHFDDDELW	SLGKGVVVPT	RFGNADGAAC	HFPFIFEGRS
250	260	270	280	290	300
YSACTTDGRS	DGLPWCSTTA	NYDTDDRFGF	CPSERLYTRD	GNADGKPCQF	PFIFQGQSYS
310	320	330	340	350	360
ACTTDGRSDG	YRWCATTANY	DRDKLFGFCP	TRADSTVMGG	NSAGELCVFP	FTFLGKEYST
370	380	390	400	410	420
CTSEGRGDGR	LWCATTSNFD	SDKKWGFCDP	QGYSLFLVAA	HEFGHALGLD	HSSVPEALMY
430	440	450	460	470	480
PMYRFTEGPP	LHKDDVNGIR	HLYGPRPEPE	PRPPTTTTPQ	PTAPPTVCPT	GPPTVHPSER
490	500	510	520	530	540
PTAGPTGPPS	AGPTGPPTAG	PSTATTVPLS	PVDDACNVNI	FDAIAEIGNQ	LYLFKDGKYW
550	560	570	580	590	600
RFSEGRGSRP	QGPFLIADKW	PALPRKLDSV	FEEPLSKKLF	FFSGRQVWVY	TGASVLGPRR
610	620	630	640	650	660
LDKLGLGADV	AQVTGALRSG	RGKMLLFSGR	RLWRFDVKAQ	MVDPRSASEV	DRMFPGVPLD
670	680	690	700		
THDVFQYREK	AYFCQDRFYW	RVSSRSELNQ	VDQVGYVTYD	ILQCPED	